WHAT IS CLAIMED IS:

1. A method of enhancing inorganic carbon fixation by a photosynthetic organism, the method comprising the step of transforming cells of the photosynthetic organism with an expressible polynucleotide encoding a polypeptide having a bicarbonate transporter activity.

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2. The method of claim 1, wherein said step of transforming said cells of the photosynthetic organism with said expressible polynucleotide encoding said bicarbonate transporter is effected by a method selected from the group consisting of genetic transformation and transient transformation.

3. The method of claim 2, wherein said genetic transformation is effected by a method selected from the group consisting of Agrobaterium mediated transformation, electroporation and particle bombardment.

4. The method of claim 2, wherein said transient transformation is effected by a method selected from the group consisting of viral transformation, electroporation and particle bombardment.

5. The method of claim 1, wherein said expressible polynucleotide includes:

(i) a nucleic acid sequence corresponding to at least a portion derived from SEQ ID NO:2, said portion encodes said protein having said bicarbonate transporter activity;

(ii) a nucleic acid sequence at least 60 % identical to said portion, as determined using the Blast software where gap penalty equals 10 for existence and 10 for extension, average match equals 10 and average mismatch equals -5;

(iii) a nucleic acid segment hybridizable with said portion under hybridization conditions of hybridization solution containing 10 % dextrane sulfate, 1 M NaCl, 1 % SDS and 5 x 10^6 cpm ^{32}p labeled probe, at 65 °C, with a final wash solution of 0.2 x SSC and 0.1 % SDS and final wash at 65 ° C;

(iv) a man induced variation of said portion; or

(v) a naturally occurring variation of said portion.

6. The method of claim 1, wherein said polypeptide is at least 70 % homologous to SEQ ID NO:3 or a portion thereof having said bicarbonate transporter activity as determined using the Blast software where gap open penalty equals 11, gap extension penalty equals 1 and matrix is blosum62.

7. The method of claim 1, wherein the photosynthetic organism is a plant.

8. The method of claim 7, wherein said plant is a C3 plant.

9. The method of claim 8, wherein said C3 plant is selected from the group consisting of tobacco, tomato, soybeans, potato, cucumber, cotton, wheat, rice and barley.

10. The method of claim 7, wherein said plant is a C4 plant.

11. The method of claim 10, wherein said C4 plant is selected from the group consisting of corn, sugar cane and sorghum.

12. The method of claim 1, wherein said polynucleotide further includes a plant promoter.

13. The method of claim 12, wherein said plant promoter is selected from the group consisting of a constitutive plant promoter, a tissue specific plant promoter and an inducible plant promoter.

14. The method of claim 13, wherein:

(i) said constitutive plant promoter is independently selected from the group consisting of CaMV35S plant promoter, CaMV19S plant promoter, FMV34S plant promoter, sugarcane bacilliform badnavirus plant promoter, CsVMV plant promoter, *Arabidopsis* ACT2/ACT8 actin plant promoter, *Arabidopsis* ubiquitin UBQ1 plant promoter, barley leaf thionin BTH6 plant promoter, and rice actin plant promoter;

(ii) said tissue specific plant promoter is independently selected from the group consisting of bean phaseolin storage protein plant promoter, DLEC plant promoter, PHSβ plant promoter, zein storage protein plant promoter, conglutin gamma plant promoter from soybean, AT2S1 gene plant promoter, ACT11 actin plant promoter from *Arabidopsis*, napA plant promoter from *Brassica napus* and potato patatin gene plant promoter; and

(iii) said inducible plant promoter is independently selected from the group consisting of a light-inducible plant promoter derived from the pea rbcS gene, a plant promoter from the alfalfa rbcS gene, DRE, MYC and MYB plant promoters which are active in drought; INT, INPS, prxEa, Ha hsp17.7G4 and RD21 plant promoters active in high salinity and osmotic stress, and hsr203J and str246C plant promoters active in pathogenic stress.

15. The method of claim 1, wherein said polynucleotide further includes a sequence element selected from the group consisting of a

nucleic acid sequence encoding a transit peptide, an origin of replication for propagation in bacterial cells, at least one sequence element for integration into a plant's genome, a polyadenylation recognition sequence, a transcription termination signal, a sequence encoding a translation start site, a sequence encoding a translation stop site, plant RNA virus derived sequences, plant DNA virus derived sequences, tumor inducing (Ti) plasmid derived sequences and a transposable element derived sequence.

16. A nucleic acid molecule for enhancing inorganic carbon fixation by a photosynthetic organism, the nucleic acid molecule comprising a polynucleotide encoding a polypeptide having a bicarbonate transporter activity.

17. The nucleic acid molecule of claim 16, further comprising a plant promoter being upstream to the polynucleotide effective in expressing said polypeptide in a plant.

18. The nucleic acid molecule of claim 16, wherein said polynucleotide includes:

(i) a nucleic acid sequence corresponding to at least a portion derived from SEQ ID NO:2, said portion encodes said protein having said bicarbonate transporter activity;

(ii) a nucleic acid sequence at least 60 % identical to said portion, as determined using the Blast software where gap penalty equals 10 for existence and 10 for extension, average match equals 10 and average mismatch equals -5;

(iii) a nucleic acid segment hybridizable with said portion under hybridization conditions of hybridization solution containing 10 % dextrane sulfate, 1 M NaCl, 1 % SDS and 5 x 10^6 cpm ^{32}p labeled probe, at 65 °C, with a final wash solution of 0.2 x SSC and 0.1 % SDS and final wash at 65 ° C;

(iv) a man induced variation of said portion; or

(v) a naturally occurring variation of said portion.

19. The nucleic acid molecule of claim 16, wherein said polypeptide is at least 70 % homologous to SEQ ID NO:3 or a portion thereof having said bicarbonate transporter activity as determined using the Blast software where gap open penalty equals 11, gap extension penalty equals 1 and matrix is blosum62.

20. The nucleic acid molecule of claim 17, wherein said plant promoter is selected from the group consisting of a constitutive plant promoter, a tissue specific plant promoter and an inducible plant promoter.

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21. The nucleic acid molecule of claim 20, wherein:

(i) said constitutive plant promoter is independently selected from the group consisting of CaMV35S plant promoter, CaMV19S plant promoter, FMV34S plant promoter, sugarcane bacilliform badnavirus plant promoter, CsVMV plant promoter, *Arabidopsis* ACT2/ACT8 actin plant promoter, *Arabidopsis* ubiquitin UBQ1 plant promoter,

barley leaf thionin BTH6 plant promoter, and rice actin plant promoter;

(ii) said tissue specific plant promoter is independently selected from the group consisting of bean phaseolin storage protein plant promoter, DLEC plant promoter, PHSβ plant promoter, zein storage protein plant promoter, conglutin gamma plant promoter from soybean, AT2S1 gene plant promoter, ACT11 actin plant promoter from *Arabidopsis*, napA plant promoter from *Brassica napus* and potato patatin gene plant promoter; and

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(iii) said inducible plant promoter is independently selected from the group consisting of a light-inducible plant promoter derived from the pea rbcS gene, a plant promoter from the alfalfa rbcS gene, DRE, MYC and MYB plant promoters which are active in drought; INT, INPS, prxEa, Ha hsp17.7G4 and RD21 plant promoters active in high salinity and osmotic stress, and hsr203J and str246C plant promoters active in pathogenic stress.

22. The nucleic acid molecule of claim 16, further comprising a sequence element selected from the group consisting of an origin of replication for propagation in bacterial cells, at least one sequence element for integration into a plant's genome, a polyadenylation recognition sequence, a transcription termination signal, a sequence encoding a translation start site, a sequence encoding a translation stop site, plant RNA virus derived sequences, plant DNA virus derived sequences, tumor inducing (Ti) plasmid derived sequences and a transposable element derived sequence.

23. A transformed photosynthetic organism comprising the nucleic acid molecule of claim 16.

24. A transformed photosynthetic organism comprising the nucleic acid molecule of claim 17.

25. The transformed photosynthetic organism of claim 16, wherein the photosynthetic organism is a plant.

26. The transformed photosynthetic organism of claim 25, wherein said plant is a C3 plant.

27. The transformed photosynthetic organism of claim 26, wherein said C3 plant is selected from the group consisting of tobacco, tomato, soybeans, potato, cucumber, cotton, wheat, rice and barley.

28. The transformed photosynthetic organism of claim 25, wherein said plant is a C4 plant.

29. The transformed photosynthetic organism of claim 28, wherein said C4 plant is selected from the group consisting of corn, sugar cane and sorghum.

30. The transformed photosynthetic organism of claim 23, wherein said organism is characterized by a photosynthetic rate at least 10 % higher as compared to a control non-transformed organism under otherwise identical conditions.